

SEQUENCE LISTING

<110> Brenda F. Baker
Susan M. Freier

<120> ANTISENSE MODULATION OF INTERLEUKIN 8 EXPRESSION

<130> RTS-0266

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09950143-092401

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096043.09240
FOI260-240960

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 aaccattctc actgtgtgta aac atg act tcc aag ctg gcc gtg gct ctc ttg 1613

Met Thr Ser Lys Leu Ala Val Ala Leu Leu

1

5

10

gca gcc ttc ctg att tct gca gct ctg tgt gaa ggt aag cac atc ttt 1661
 Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Lys His Ile Phe

15

20

25

T04260 E409660

00000113 00000001

tat tga cca gat aaa aat acc atg aag atg ttg ata ttg tac aaa aag 2237
 Tyr * Pro Asp Lys Asn Thr Met Lys Met Leu Ile Leu Tyr Lys Lys
 195 200 205

aac tct aac tct tat ata gga agt tgt tca atg ttg tca gtt atg act 2285
 Asn Ser Asn Ser Tyr Ile Gly Ser Cys Ser Met Leu Ser Val Met Thr
 210 215 220

gtt ttt taa aac aaa gaa cta act gag gtc aag ggc tag gag ata ttc 2333
 Val Phe * Asn Lys Glu Leu Thr Glu Val Lys Gly * Glu Ile Phe
 225 230 235

agg aat gag ttc act aga aac atg atg cct tcc ata gtc tcc aaa taa 2381
 Arg Asn Glu Phe Thr Arg Asn Met Met Pro Ser Ile Val Ser Lys *
 240 245 250

tca tat tgg aat tag aag gaa gta gct ggc aga gct gtg cct gtt gat 2429
 Ser Tyr Trp Asn * Lys Glu Val Ala Gly Arg Ala Val Pro Val Asp
 255 260 265

aaa atc aat cct taa tca ctt ttt ccc cca aca ggt gca gtt ttg cca 2477
 Lys Ile Asn Pro * Ser Leu Phe Pro Pro Thr Gly Ala Val Leu Pro
 270 275 280

agg agt gct aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa 2525
 Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys
 285 290 295

cct ttc cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga 2573
 Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly
 300 305 310

cca cac tgc gcc aac aca gaa att atg taa gta ctt taa aaa aga tta 2621
 Pro His Cys Ala Asn Thr Glu Ile Met * Val Leu * Lys Arg Leu
 315 320 325

gat att ttg ttt tag caa act taa aat taa gga agg tgg aaa tat tta 2669
 Asp Ile Leu Phe * Gln Thr * Asn * Gly Arg Trp Lys Tyr Leu
 330 335

gga aag ttc cag gtg tta gga tta cag tag taa atg aaa caa aac aaa 2717
 Gly Lys Phe Gln Val Leu Gly Leu Gln * * Met Lys Gln Asn Lys
 340 345 350

0950143 092401

ata aaa ata ttt gtc tac atg aca ttt aaa tat ggt agc ttc cac aac 2765
 Ile Lys Ile Phe Val Tyr Met Thr Phe Lys Tyr Gly Ser Phe His Asn
 355 360 365

tac tat aaa tgt tat ttt gga ctt aga ctt tat gcc tga ctt aag gaa 2813
 Tyr Tyr Lys Cys Tyr Phe Gly Leu Arg Leu Tyr Ala * Leu Lys Glu
 370 375 380

tca tga ttt gaa tgc aaa aac taa ata tta atc tga acc att tct ttc 2861
 Ser * Phe Glu Cys Lys Asn * Ile Leu Ile * Thr Ile Ser Phe
 385 390 395

tta ttt cag tgt aaa gct ttc tga tgg aag aga gct ctg tct gga ccc 2909
 Leu Phe Gln Cys Lys Ala Phe * Trp Lys Arg Ala Leu Ser Gly Pro
 400 405 410

caa gga aaa ctg ggt gca gag ggt tgt gga gaa gtt ttt gaa gag gta 2957
 Gln Gly Lys Leu Gly Ala Glu Gly Cys Gly Glu Val Phe Glu Glu Val
 415 420 425

agt tat ata ttt ttt aat tta aat ttt tca ttt atc ctg aga cat ata 3005
 Ser Tyr Ile Phe Phe Asn Leu Asn Phe Ser Phe Ile Leu Arg His Ile
 430 435 440

atc caa agt cag cct ata aat ttc ttt ctg ttg cta aaa atc gtc att 3053
 Ile Gln Ser Gln Pro Ile Asn Phe Phe Leu Leu Leu Lys Ile Val Ile
 445 450 455 460

agg tat ctg cct ttt tgg tta aaa aaa aag gaa tag cat caa tag tga 3101
 Arg Tyr Leu Pro Phe Trp Leu Lys Lys Lys Glu * His Gln * *
 465 470

gtt tgt tgt act tat gac cag aaa gac cat aca tag ttt gcc cag gaa 3149
 Val Cys Cys Thr Tyr Asp Gln Lys Asp His Thr * Phe Ala Gln Glu
 475 480 485

att ctg ggt tta agc ttg tgt cct ata ctc tta gta aag ttc ttt gtc 3197
 Ile Leu Gly Leu Ser Leu Cys Pro Ile Leu Leu Val Lys Phe Phe Val
 490 495 500

act ccc agt agt gtc cta ttt tag atg ata att tct ttg atc tcc cta 3245
 Thr Pro Ser Ser Val Leu Phe * Met Ile Ile Ser Leu Ile Ser Leu
 505 510 515

09960443-09960441
 09960440-09960441

ttt ata gtt gag aat ata gag cat ttc taa cac atg aat gtc aaa gac 3293
 Phe Ile Val Glu Asn Ile Glu His Phe * His Met Asn Val Lys Asp
 520 525 530

tat att gac ttt tca aga acc cta ctt tcc ttc tta tta aac ata gct 3341
 Tyr Ile Asp Phe Ser Arg Thr Leu Leu Ser Phe Leu Leu Asn Ile Ala
 535 540 545 550

cat ctt tat att ttt aat ttt att tta ggg ctg aga att cat aa 3385
 His Leu Tyr Ile Phe Asn Phe Ile Leu Gly Leu Arg Ile His
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104260-24709660

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